

GEPHE SUMMARY

	Gephebase Gene		GepheID
Dihydropteroate synthase (pvdhps) (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Dihydropteroate+synthase+(pvdhps)^#gephebase-summary-title)	GP00001485		
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)		Trait	
Xenobiotic resistance (sulfadoxine) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic+resistance+(sulfadoxine)^#gephebase-summary-title)		Trait State in Taxon A	
Malaria parasite - sensitive		Trait State in Taxon B	
Malaria parasite - resistant		Ancestral State	
Unknown		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Plasmodium vivax (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Plasmodium+vivax^#gephebase-summary-title)	Latin Name	Plasmodium vivax (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Plasmodium+vivax^#gephebase-summary-title)	Latin Name
malaria parasite P. vivax	Common Name	malaria parasite P. vivax	Common Name
Haemamoeba vivax; malaria parasite P. vivax	Synonyms	Haemamoeba vivax; malaria parasite P. vivax	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	Lineage	cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	Lineage
Plasmodium (Plasmodium) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103)	Parent	Plasmodium (Plasmodium) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103)	Parent
5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855)	NCBI Taxonomy ID	5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855)	NCBI Taxonomy ID
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Plasmodium vivax
DHPS		Q00LX9 (http://www.uniprot.org/uniprot/Q00LX9)	
-	Synonyms	JN794522.1 (https://www.ncbi.nlm.nih.gov/nuccore/JN794522.1)	GenebankID or UniProtKB
-	String		
-	Sequence Similarities		
GO:0004156 : dihydropteroate synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004156)	GO - Molecular Function		
GO:0042558 : pteridine-containing compound metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0042558)	GO - Biological Process		
-	GO - Cellular Component		
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Unknown^#gephebase-summary-title)			Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Unknown^#gephebase-summary-title)			Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping~#gephebase-summary-title)	Experimental Evidence
Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . (2016) (https://pubmed.ncbi.nlm.nih.gov/27348299)	Main Reference
Pearson RD; Amato R; Auburn S; Miotto O; Almagro-Garcia J; Amaratunga C; Suon S; Mao S; Noviyanti R; Trimarsanto H; Marfurt J; Anstey NM; William T; Boni MF; Dolecek C; Hien TT; White NJ; Michon P; Siba P; Tavul L; Harrison G; Barry A; Mueller I; Ferreira MU; Karunaweera N; Randrianarivelosia M; Gao Q; Hubbart C; Hart L; Jeffery B; Drury E; Mead D; Kekre M; Campino S; Manske M; Cornelius VJ; MacInnis B; Rockett KA; Miles A; Rayner JC; Fairhurst RM; Nosten F; Price RN; Kwiatkowski DP	Authors
The widespread distribution and relapsing nature of <i>Plasmodium vivax</i> infection present major challenges for the elimination of malaria. To characterize the genetic diversity of this parasite in individual infections and across the population, we performed deep genome sequencing of >200 clinical samples collected across the Asia-Pacific region and analyzed data on >300,000 SNPs and nine regions of the genome with large copy number variations. Individual infections showed complex patterns of genetic structure, with variation not only in the number of dominant clones but also in their level of relatedness and inbreeding. At the population level, we observed strong signals of recent evolutionary selection both in known drug resistance genes and at new loci, and these varied markedly between geographical locations. These findings demonstrate a dynamic landscape of local evolutionary adaptation in the parasite population and provide a foundation for genomic surveillance to guide effective strategies for control and elimination of <i>P. vivax</i> .	Abstract
	Additional References

RELATED GEPHE

5 (ABC transporter pvmp1, Dihydrofolate reductase (pvdhfr), Multidrug resistance protein 1 (pvmdr1), PVX_084940, PVX_101445) (https://www.gephebase.org/search-criteria?/or+Taxon+ID=~5855~/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

With strong evidence of recent selection in western Thailand. The signal of selection encompasses multiple genes such that we cannot be certain of the specific gene under selection. A noteworthy candidate also observed in selective sweeps in South America